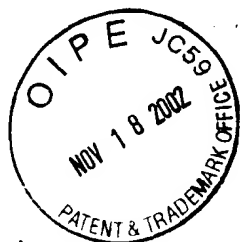




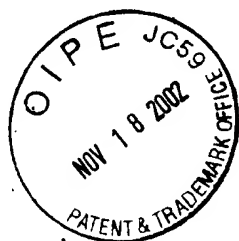
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eLeuMETMET AlaAsnValPhe IleTyrLeu IleValGlu
81 GTCTCCAAAA ACAGTAGCCA AGACAAAAAT GGAAAGGGAG
ValSerLysAsn SerSerGln AspLysAsn GlyLysGlyG
121 GAGTAATAAT CCGAAAGAG AAGTTCTGGA AGCCACCCAG
lyValIleIle ProLysGlu LysPheTrpLys ProProSe
161 CACTCCCCCG GCATCTGGA ACAGGGAACA GGAGAAGCTG
rThrProArg AlaTyrTrpAsn ArgGluGln GluLysLeu
201 AACAGGIGGT ACAATCCCAT CTGAACAGG GTGGCCAATC
AsnArgTrpTyr AsnProIle LeuAsnArg ValAlaAsnG
241 AGACAGGGGA GCTAGCCACA TCTCCAAACA CAAGTCACCT
InThrGlyGlu LeuAlaThr SerProAsnThr SerHisLe
281 GAGCTATTGT GAACAGACT CGACGGTCAT GACAGCTGTG
uSerTyrCys GluProAspSer ThrValMET ThrAlaVal
321 ACAGATTTTA ATAATCTGCC GGACAGATTT AAAGACTTTC
ThrAspPheAsn AsnLeuPro AspArgPhe LysAspPheL
361 TCTTGATTTT GAGATGCGCG AATTACTGCG TGCTTATAGA
euLeuTyrLeu ArgCysArg AsnTyrSerLeu LeuIleAs
401 TCAACCGAAG AATGTGCAA AGAAGCCCTT CTACTATTG
pGlnProLys LysCysAlaLys LysProPhe LeuLeuLeu
441 GCGATAAAGT CCTCATTC ACATTTTGCC AGAAGGCAAG
AlaIleLysSer LeuIlePro HisPheAla ArgArgGlnA
481 CAATTGCGGA GTCTTGGGCG CGAGAAACA ACGTAGGGAA
laIleArgGlu SerTrpGly ArgGluThrAsn ValGlyAs
521 CCAGACAGTA GTGAGGGTCT TCTGTGTCGG CAAGACACCC
nGlnThrVal ValArgValPhe LeuLeuGly LysThrPro
561 CCAGAGGACA ACCACCTGA CCTTTGGGAC ATGCTTAAGT
ProGluAspAsn HisProAsp LeuSerAsp METLeuLysP
601 TTGAGAGTGA CAAGCACCAG GACATCTCA TGTTGGAATA
heGluSerAsp LysHisGln AspIleLeuMET TrpAsnTyr
641 TAGAGACACA TTCTTCAACC TGTCCTGAA GGAAGTGCTG
rArgAspThr PhePheAsnLeu SerLeuLys GluValLeu

FIG. 1A



681 TTTCCTAGGT GGGTGAGCAC TTCTGTCCA GAAGCAGAGT
PheLeuArgTrp ValSerThr SerCysPro AspAlaGluP
721 TTGCTCTCAA GGGCGATGAT GAAGGTTTG TGAACACCCA
heValPheLys GlyAspAsp AspValPheVal AsnThrHi
761 TCACATCCTT AATTACTTGA ATAGCTTATC CAAGAGCAAA
sHisIleLeu AsnTyrLeuAsn SerLeuSer LysSerLys
801 GCCAAGACT TGTTCTATAGG TGAAGTGATC CACAATGCTG
AlaLysAspLeu PheIleGly AspValIle HisAsnAlaG
841 GGCTCACC GGATAAGAAA CTGAAGTACT ACATCCAGA
lyProHisArg AspLysLys LeuLysTyrTyr IleProGl
881 AGTCTTCTAC ACGGGGTCTT ACGCACCGTA TCGCGGGGT
uValPheTyr ThrGlyValTyr ProProTyr AlaGlyGly
921 GGTGGATTCC TGTACTCCCG CCCCCTTGGC TTGAGGCTGT
GlyGlyPheLeu TyrSerGly ProLeuAla LeuArgLeuT
961 ACAGTGGGAC TAGCGGGGTC CATCTCTACC CTATTGATGA
yrSerAlaThr SerArgVal HisLeuTyrPro IleAspAs
1001 TGTTTATACG GGAATGTGCC TTCAGAACT GGGCCTTGTT
pValTyrThr GlyMETCysLeu GlnLysLeu GlyLeuVal
1041 CCAGAGAAGC ACAAAGGCTT CAGGACATTG GATATTGAAG
ProGluLysHis LysGlyPhe ArgThrPhe AspIleGluG
1081 AGAAAAATAA GAAAAATATT TGTTCCTATA TAGACCTAAT
luLysAsnLys LysAsnIle CysSerTyrIle AspLeuME
1121 GTTAGTACAT AGCAGAAAAC CTCAAGAGAT GATTGATATC
TLeuValHis SerArgLysPro GlnGluMET IleAspIle
1161 TGGTCTCAGT TGCAAAGTCC TAATTTAAAA TGCTGA
TrpSerGlnLeu GlnSerPro AsnLeuLys Cys

FIG. 1B



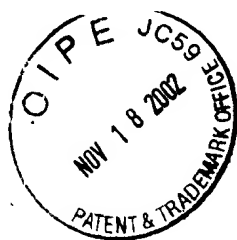
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MA - - - S SC - - - - - Y - - - - - V
MAP - - - - - AVL TAL PNRMS S L S KWSL
MQSKH R L - - - - - L C L - - - V
MLQWR R R H C C FAKMTWNAKRS I F T H I G V
LSLVXLXXXFXFLXH - - W - - - - -
40 50 60
LGILMMANV I Y I VEVSKNSSQDKNGKGG
LSVVC - - - - - A S A - - - - -
L - - - - L S L S V - - - - -
LPLILLVDYCGLT H L H - - - - -
LSLVFI L F A M L F F N H D L P G R A G F K E N P V
- - - F - - - F - - - P - - - - - I W Y
70 80 90
VIIPKEK W K P STPRAYWNREQEKLNR W Y
- - - - - - - - - - - L W Y
- - - - - - - - - - - I W Y
ELN F E R H F H Y - - - - -
TYT F R G - F R S T K S E T N H S S L R - - - - - N I W K
LSIP - - LRPQTGSXSXSXXLSHL - Y - - - - N
100 110 120
NPILNRVAN T E L A T P N T S H L S Y C E P D S
LSIT - - - F E - S Y T G K P F S H I - - - - -
LSL P H Y - - - - -
- - - - - L N D D T G G G A F S G L D K F A V - - - - -
ETV F Q T L R P O T A T N S N N T D L S P Q G V T G L E N
TVXRXXNXFXFNXXTR - - - - - P I N S X X F E F
130 140 150
TVM T A V T D F N N L P D F F K D F L L Y L R C R N Y S L
TVA R K N F T F G M I R P P - - - - - P I N P H S F F F
VIE P V E W M Y F - Y E Y E - - - - - P I Y R Q D F R F
- - - - - L R V P S F T A F V
T L S A N G S I Y N E K G I G - - - - - H P N S Y H F K Y
L I D E P X K C X K K - P F L V L L I K S X P G X F X A R Q
160 170 180

FIG. 2A



160 170 180
L I P Q F K A H - P L A L I P H A R
L I N E N E N I I S T H K E D
T L R H S N S H Q N I V T R S D V K A
P V Q A R - - - - - T M A V N S R R E
I N F E Q E S I A A E Q I E R
A I R E T W G X E X N F X G I X V X R V F L L G K X A - E X
190 200 210
A I R E S W G R E T N V G N O T V V F L L G F T P P E D
A I R E T W G D E N H F K K I A T L F L L G P N A - - -
A I P V T W G E K K S W W C Y E V L T F F L L G Q Q A - E R
A I P R T W G Y E G R E S D V H L R E V F L L G T A E D S E
A I P Q T W G N F S L A P Q I T E I F L L G L S I - - K
X D P X L X X M V E X E S R X H G D I I Q Q D F L D T Y F N
220 230 240
N H E D L S D M L K F E S D K Q D I L M W N Y R D T F F
- D F V L N Q M V E Q E S Q I F H D I I V E D F I C S Y H
E D K T A L S L E D E H V L Y J D I I R D D F I D T Y N
K - - - - - V A W E S H E H G D I L A D F T D A Y E
L N G Y I Q R A I L E E S F Q Y H D I I Q C E Y L D T Y Y
L T L K T L M G M R W V A T F C P X A E Y V M K T D S D V F
250 260 270
S L K E V L F L R W V S I S D A F F F F G D D D V F
L T L K T L M G M R W V A T F C S K A K Y V M K T D S D I
L T L K T I M A F R W V M E F C I N A K Y I M K T D T D V F
N T L K T M L G M R W A S E Q F N R S F Y L F V E D D Y Y
L T I K T L M G M N W V A T Y D I H I P Y V M K T D S D M E
V N T X N L L N K L L K P S L S H R X X L F T G Y - V I X G
280 290 300
N T H H I L N Y L N S L S K K A K D F I C - D V I H N
N M D N L I Y L L F F S T K P R R Y F T G Y - V I N
I T G N I V K Y L I - - N N S E K F F T G Y P L I D N
S A K N V K F L G R G R O P E L F A G H V F Q T
N T E Y L I N F L I R E D P P H N Y F T G Y - L M R

FIG. 2B



YGPXRDKFSKWIYPXDLYPF XVYPPYCSGG
310 320 330
AGFHRDRLKL Y EVF T-G PPAAGS
-GEIRVR M R DSN PIFCSCT
MS-YFGFHHNH SYQEYPK FPPYCSGL
-SLFHKFSKWIYVSLEEYPERDRWPPYVTA
YAFNENEDSKWYM PPLYE SER YPVF T
GYIFSGDLAERLYKASLHVRLLLHLEDVYVG
340 350 360
FLYSCPLAL EYS TSR H YPIDVYT
GYIFSGADV LI T T EDVYV
GYIMSGDIVP V EMMS KPIKFEDVYV
AFLLSQKALRQ A V LP FRFDVYL
YVVSGLL KIF V GI R EDVYV
ICLXKLGIDPXXPXG - - - FNHW - KXXKSXC
370 380 390
MCLQKLGVL EKHKG FRT FDIEEANKENIC
LCLRKLGLH EFONS - - - FNHW - FMAYLC
ICINLIKVI IHIE EDTNL FFLY - RIHLDV
IVALAGISLQHCDD - - - FRFHRPAY GPD
CIAFIRIDEVP PNEFV FNHW - RVSY S
SYSRVIAVHQF - SPEEMIRIWNXL - Q - KNL
400 410 420
YIDLMLVHSR - KQEMIDIWSQL - SP
RYRRVITVH I - SPEEMHPIWIDMSSSK H
QLRPIVIAAHG - SKEITFQVML - - R T
YSSVIAASH EFGDPEMTVWLE - - -
KYSHLITSHCE - QESPLIKYWNH Q N HN
XC - - - - - Y - - - -
430
KC .
RC
TC - - - - - HY
- C - - - - - RSANY - - - - A
A C ANAAKEKAGRY RHRKLH

FIG. 2C

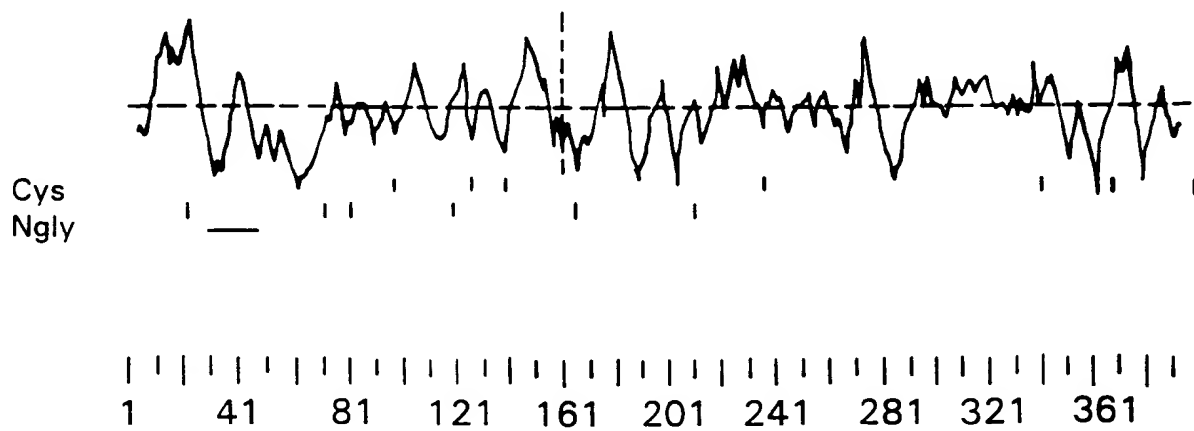


FIG. 3

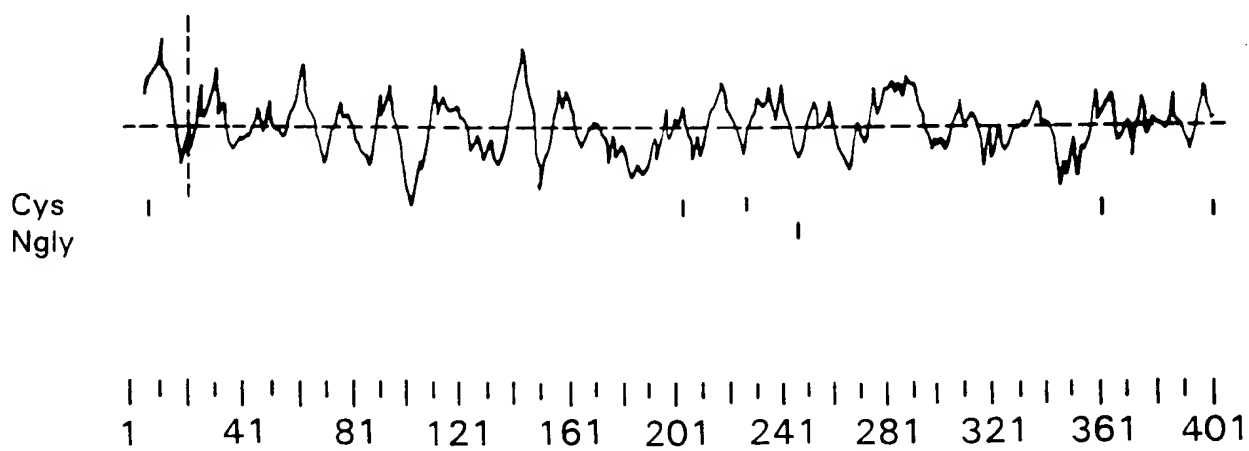
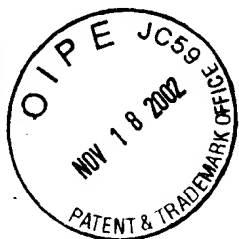
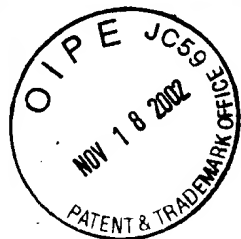


FIG. 5



1 ATGATTIGOC CTCAGCTTT ACTGGTTATT TTAAGAAATT
METIleCysPro SerAlaLeu LeuValIle LeuArgAsnL
41 TAATAACGGGA AGAAAAATC ATTTCTCAAG AGATCCTCAA
euIleArgGlu GluLysIle IleSerGlnGlu IleLeuAs
81 TTTGATTGAA TTAAGGATGA AAAAAGGGAA TATTCAGTTG
nLeuIleGlu LeuArgMETLys LysGlyAsn IleGlnLeu
121 ACAAACTCTG CAATCAGTGA TGCATTAAAA GAAATCGATA
ThrAsnSerAla IleSerAsp AlaLeuLys GluIleAspS
161 GTAGTGTGCT CAATGTTCCT GTCAACGGGG AGACGGGATC
erSerValLeu AsnValAla ValThrGlyGlu ThrGlySe
201 AGGGAAGTCC AGCTTCATCA ATACCTGAG AGGCATTGGG
rGlyLysSer SerPheIleAsn ThrLeuArg GlyIleGly
241 AATGAAGAAG AAGGTGCAGC TAAACTCGG GTGGTGGAGG
AsnGluGluGlu GlyAlaAla LysThrGly ValValGluV
281 TAACCATGGA AAGACATCCA TACAAACACC CCAATATACC
alThrMETGlu ArgHisPro TyrLysHisPro AsnIlePr
321 CAATGIGGTT TTTTGGGACC TGCTGGGAT TGGAGGCACA
cAsnValVal PheTrpAspLeu ProGlyIle GlySerThr
361 AATTTCOCAC CAAACACTA CCTGGAGAAA ATGAAGTTCT
AsnPheProPro AsnThrTyr LeuGluLys METLysPheT
401 ATGAGTACGA TTCTTCATT ATTATTTCGG CCACAGCTT
yrGluTyrAsp PhePheIle IleIleSerAla ThrArgPh
441 CAAGAAAAAT GATATAGACA TTGCCAAAGC AATCAGCATG
eLysLysAsn AspIleAspIle AlaLysAla IleSerMET
481 ATGAAGAAGG AATTCTACTT CGTGAGAAC AAGGTGGACT
METLysLysGlu PheTyrPhe ValArgThr LysValAspS
521 CTGACATAAC AAATGAAGCA GATGGCAAAC CTCAAACCTT
erAspIleThr AsnGluAla AspGlyLysPro GlnThrPh
561 TGACAAAGAA AAGGTCTGCT AGGACATCCG CCTTAACTGT
eAspLysGlu LysValLeuGln AspIleArg LeuAsnCys
601 GTGAACACCT TTAGGGAGAA TGGCATTCCT GAGCCACCAA
ValAsnThrPhe ArgGluAsn GlyIleAla GluProProI
641 TCTTCTGCT CTCTAACAAA AATGTTTGTC ACTATGACTT
lePheLeuLeu SerAsnLys AsnValCysHis TyrAspPh

FIG. 4A



681 CCCCCTCCTG ATGGACAAGC TGATAAGTGA CCTCCCTATC
eProValLeu METAspLysLeu IleSerAsp LeuProIle
721 TACAGGAGAC ACAATTTTAT GGCTCCTTA CCAATATCA
TyrArgArgHis AsnPheMET ValSerLeu ProAsnIleT
761 CAGATTTCAGT CATTGAAAAG AAGCGGCAAT TTCTGAAGCA
hrAspSerVal IleGluLys LysArgGlnPhe LeuLysGI
801 RAGGATTTGG CTGGAAGGAT TTGCTGCTGA CCTAGTGAAT
nArgIleTrp LeuGluGlyPhe AlaAlaAsp LeuValAsn
841 ATCATCCCTT CTCGACCTT TCTCTGGAC AGTGATTGG
IleIleProSer LeuThrPhe LeuLeuAsp SerAspLeuG
881 AGACTCTGAA GAAAGCATG AAATTCTAOC GCACTGIGTT
luThrLeuLys LysSerMET LysPheTyrArg ThrValPh
921 TGGAGTGCAT GAAACATCTT TGCAGAGATT AGCTAGGGAC
eGlyValAsp GluThrSerLeu GlnArgLeu AlaArgAsp
961 TGGGAAATAG AGGTGGATCA GGTGGAGGCC ATGATAAAAT
TrpGluIleGlu ValAspGln ValGluAla METIleLysS
1001 CTCCTGCTGT GTTCAAACCT ACAGATGAAG AAACAATACA
erProAlaVal PheLysPro ThrAspGluGlu ThrIleGI
1041 AGAAAGGCCTT TCAAGATATA TTCAGGAGTT CIGTTTGGCT
nGluArgLeu SerArgTyrIle GlnGluPhe CysLeuAla
1081 AATGGGTACT TACTTCTAA AAATAGTTTT CTAAAGAAA
AsnGlyTyrLeu LeuProLys AsnSerPhe LeuLysGluI
1121 TATTTTACCT GAAATATTAT TTCTTGACA TGGTGACTGA
lePheTyrLeu LysTyrTyr PheLeuAspMET ValThrGI
1161 GGATGCTAAA ACTCTTCTTA AAGAGATATG TTTAAGAAAC
uAspAlaLys ThrLeuLeuLys GluIleCys LeuArgAsn
1201 TAG

FIG. 4B

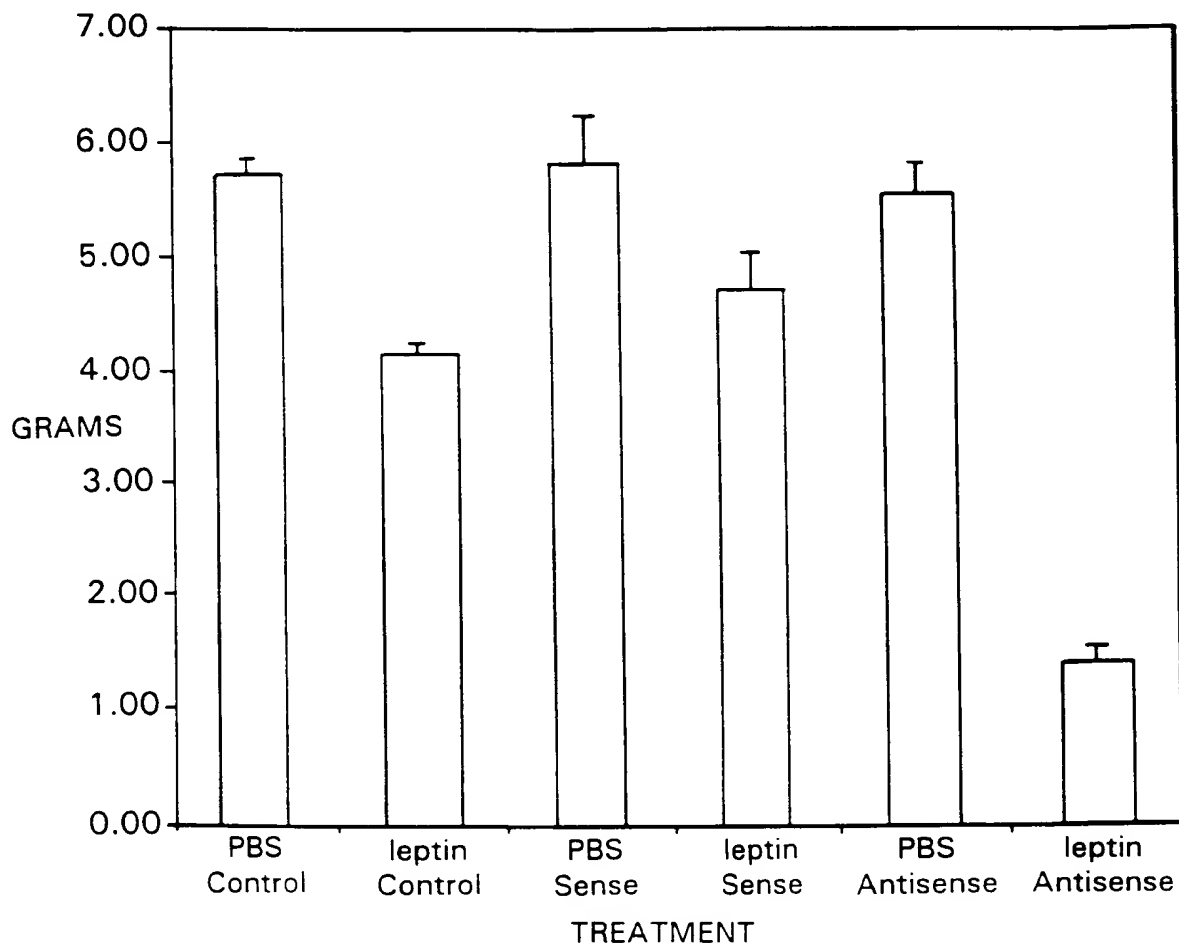
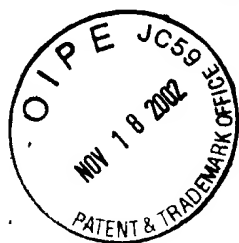


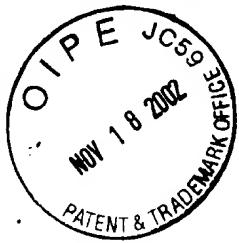
FIG. 6



5'

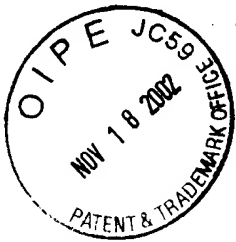
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GCGGAGCGGCCGGGACGTGGATGTGGCCGCGATCTCCCGCCCTTGCCCCCGC
CCCGCCGAGCTGGAGCTGCTCCCGGACAAGATATGAGAAATGAGTGTTGGA
CGTCGAAGAATAAAGTTGTTGGGTATCCTGATGATGGCAAATGTCTTCATTTA
TTTTATTATGGAAGTCTCCAAAAGCAGTAGCCAAGAAAAAATGGAAAAGGG
GAAGTAATAATACCCAAAGAGAAGTTCTGGAAGATATCTACCCCTCCCGAGG
CATACTGGAACCGAGAGCAAGAGAAGCTGAACCGGCAGTACAACCCCATCCT
GAGCATGCTGACCAACCAGACGGGGGAGGCGGGCAGGCTCTCCAATATAAG
CCATCTGAACTACTGCGAACCTGACCTGAGGGTCACGTCCGTGGTTACGGGT
TTTAACAACCTTGCCGGACAGATTTAAAGACTTTCTGCTGTATTTGAGATGCCG
CAATTATTCAGTCTTATAGATCAGCCGGATAAGTGTGCAAAGAAACCTTTCT
TGTTGCTGGCGATTAAAGTCCCTCACTCCACATTTTGCCAGAAGGC.AAGCAATC
CGGGAATCCTGGGGCCAAGAAAGCAACGCAGGGAACC.AAACGGTGGTGCGA
GTCTTCCTGCTGGGCCAGACACCCCCAGAGGACAACC.ACCCCGACCTTTCAG
ATATGCTGAAATTTGAGAGTGAGAAGCACCAAGACATTCTTATGTGGAACTA
CAGAGACACTTTCTTCAACTTGTCTCTGAAGGAAGTGCTGTTTCTCAGGTGGG
TAAGTACTTCCTGCCCAGACACTGAGTTTGTGTTTCAAGGGCGATGACGATGTT
TTTGTGAACACCCATCACATCCTGAATTACTTGAATAGTTTATCCAAGACCAA
AGCCAAAGATCTCTTCATAGGTGATGTGATCCACAATGCTGGACCTCATCGG
GATAAGAAGCTGAAGTACTACATCCCAGAAGTTGTTTACTCTGGCCTCTACCC
ACCCTATGCAGGGGGAGGGGGGTTCTCTACTCCGGCCACCTGGCCCTGAGG
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FIG. 7A



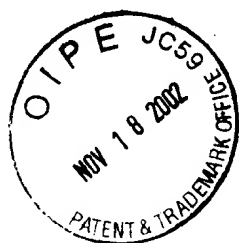
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CAGTTGCAGAGTGCTCATTTAAAATGCTAAAATAGATACAACTCAATTTKG
SATWGRAAGGGGTWTTTTGRATWGGYCCCATGTTGGGGTCTCACATTAGAGT
AATTTCTATTTNAANCATGAAATTGCCTTTATGAGTGATACCCATTTANGGCC
TCTAANCCTTCATTTGNACTCACGTGAAGAAGGGAAAGCGGGAGAAGGTAAT
TTNTTTATGGTGAATGGCAGGATATTGGTCTGACTTACCGNTAGGGGANTTTA
AAACTGGNCCTTTTTGAATCTGTTTGGATGGCCCTT

FIG. 7B



MSVGRRRIKLLGILMMANVFIYFIMEVSKSSSQEKNGKGEVIIPKEKFWKISTPPE
AYWNREQEKLNRQYNPILSMLTNQTGEAGRLSNISHLNYCEPDLRVTSVVTGFN
NLPDRFKDFLLYLRCRNYSLIDQPDKCAKKPFLLLAIKSLTPHFARRQAIRESWG
QESNAGNQTVVRVFLLGQTPPEDNHPDLSDMLKFESEKHQDILMWNRYRDTFFNL
SLKEVLFLRWVSTSCPDTEFVFKGDDDVFNTHHILNYLNSLSKTKAKDLFIGDV
IHNA GPHRDKKLKYYTPEVVYSGLYPPYAGGGGFLYSGHLALRLYHITDQVHLY
PIDDVYTGMCLOKLGLVPEKHKGFRTFDIEEKNKNNICSYVDLMLVHSRKPQEM
IDIWSQLQSAHLKC

FIG. 8



246 ATGAGTGTGGACGTCGAAGAATAAAGTTGTTG--GG-TATCCTGATGATGGCAAATGTC 302
|||||
1 ATGAGTGTGGACGTCGAAGAATAAAGTTGTTGTTGGGTATCCTGATGATGGCAAATGTC 60

303 TTCATTTATTTTATTATGGAAGTCTCCAAAAGCAGTAGCCAAGAAAAAATGGAAAAGGG 362
|||||
61 TTCATTTATTTTATTATGGAAGTCTCCAAAAGCAGTAGCCAAGAAAAAATGGAAAAGGG 120

363 GAAGTAATAATACCCAAAGAGAAGTTCTGGAAGATATCTACCCCTCCCGAGGCATACTGG 422
|||||
121 GAAGTAATAATACCCAAAGAGAAGTTCTGGAAGATATCTACCCCTCCCGAGGCATACTGG 180

423 AACCGAGAGCAAGAGAAGCTGAACCGGCAGTACAACCCCATCCTGAGCATGCTGACCAAC 482
|||||
181 AACCGAGAGCAAGAGAAGCTGAACCGGCAGTACAACCCCATCCTGAGCATGCTGACCAAC 240

483 CAGACGGGGGAGGCGGGCAGGCTCTCCAATATAAGCCATCTGAACTACTGCGAACCTGAC 542
|||||
241 CAGACGGGGGAGGCGGGCAGGCTCTCCAATATAAGCCATCTGAACTACTGCGAACCTGAC 300

543 CTGAGGGTCACGTCGGTGGTTACGGGTTTTAACAACTTGCCGGACAGATTTAAAGACTTT 602
|||||
301 CTGAGGGTCACGTCGGTGGTTACGGGTTTTAACAACTTGCCGGACAGATTTAAAGACTTT 360

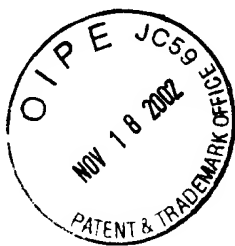
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|||||
361 CTGCTGTATTTGAGATGCCGCAATTATTCAGTCTTATAGATCAGCCGGATAAGTGTGCA 420

663 AAGAAACCTTTCTTGTTGCTGGCGATTAAGTCCCTCACTCCACATTTTGCCAGAAGGCAA 722
|||||
421 AAGAAACCTTTCTTGTTGCTGGCGATTAAGTCCCTCACTCCACATTTTGCCAGAAGGCAA 480

723 GCAATCCGGGAATCCTGGGGCCAAGAAAGCAACGCAGGGAACCAAACGGTGGTGCGAGTC 782
|||||
481 GCAATCCGGGAATCCTGGGGCCAAGAAAGCAACGCAGGGAACCAAACGGTGGTGCGAGTC 540

783 TTCCTGCTGGGCCAGACACCCCCAGAGGACAACCACCCGACCTTTCAGATATGCTGAAA 842
|||||

FIG. 9A



541 TTCCTGCTGGGCCAGACACCCCCAGAGGACAACCACCCCGACCTTTCAGATATGCTGAAA 600

843 TTTGAGAGTGAGAAGCACCAAGACATTCTTATGTGGAACACAGAGACACTTCTTCAAC 902
|||||

601 TTTGAGAGTGAGAAGCACCAAGACATTCTTATGTGGAACACAGAGACACTTCTTCAAC 660

903 TTGTCTCTGAAGGAAGTGCTGTTTCTCAGGTGGGTAAGTACTTCCTGCCCAGACACTGAG 962
|||||

661 TTGTCTCTGAAGGAAGTGCTGTTTCTCAGGTGGGTAAGTACTTCCTGCCCAGACACTGAG 720

963 TTTGTTTTCAAGGGCGATGACGATGTTTTTGTGAACACCCATCACATCCTGAATTACTTG 1022
|||||

721 TTTGTTTTCAAGGGCGATGACGATGTTTTTGTGAACACCCATCACATCCTGAATTACTTG 780

1023 AATAGTTTATCCAAGACCAAAGCCAAAGATCTCTTCATAGGTGATGTGATCCACAATGCT 1082
|||||

781 AATAGTTTATCCAAGACCAAAGCCAAAGATCTCTTCATAGGTGATGTGATCCACAATGCT 840

1083 GGACCTCATCGGGATAAGAAGCTGAAGTACTACATCCCAGAAGTTGTTTACTCTGGCCTC 1142
|||||

841 GGACCTCATCGGGATAAGAAGCTGAAGTACTACATCCCAGAAGTTGTTTACTCTGGCCTC 900

1143 TACCCACCCTATGCAGGGGGAGGGGGGTTCTCTACTCCGGCCACCTGGCCCTGAGGCTG 1202
|||||

901 TACCCACCCTATGCAGGGGGAGGGGGGTTCTCTACTCCGGCCACCTGGCCCTGAGGCTG 960

1203 TACCATATCACTGACCAGGTCCATCTCTACCCCATTGATGACGTTTATACTGGAATGTGC 1262
|||||

961 TACCATATCACTGACCAGGTCCATCTCTACCCCATTGATGACGTTTATACTGGAATGTGC 1020

1263 CTTCAGAAACTCGGCCTCGTTCCAGAGAAACACAAAGGCTTCAGGACATTTGATATCGAG 1322
|||||

1021 CTTCAGAAACTCGGCCTCGTTCCAGAGAAACACAAAGGCTTCAGGACATTTGATATCGAG 1080

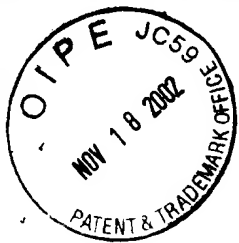
1323 GAGAAAAACAAAATAACATCTGCTCCTATGTAGATCTGATGTTAGTACATAGTAGAAAA 1382
|||||

1081 GAGAAAAACAAAATAACATCTGCTCCTATGTAGATCTGATGTTAGTACATAGTAGAAAA 1140

1383 CCTCAAGAGATGATTGATATTTGGTCTCAGTTGCAGAGTGCTCATTTAAAATGCTAA 1439
|||||

1141 CCTCAAGAGATGATTGATATTTGGTCTCAGTTGCAGAGTGCTCATTTAAAATGCTAA 1197

FIG. 9B



MSVGRRRIKLLGILMMANVFIYFIMEVSKSSSQEKNGKGEVIIPKEKFWKISTPPEAYWN
MSVGRRRIKLLGILMMANVFIYFIMEVSKSSSQEKNGKGEVIIPKEKFWKISTPPEAYWN
MSVGRRRIKLLGILMMANVFIYFIMEVSKSSSQEKNGKGEVIIPKEKFWKISTPPEAYWN

REQEKLNRQYNPILSMLTNQTGEAGRLSNISHLNYCEPDLRVTSVVTGFNNLPDRFKDFL
REQEKLNRQYNPILSMLTNQTGEAGRLSNISHLNYCEPDLRVTSVVTGFNNLPDRFKDFL
REQEKLNRQYNPILSMLTNQTGEAGRLSNISHLNYCEPDLRVTSVVTGFNNLPDRFKDFL

LYLRCRNYSLIDQPDKCAKKPFLLLAIKSLTPHFARRQAIRESWGQESNAGNQTVVVRVF
LYLRCRNYSLIDQPDKCAKKPFLLLAIKSLTPHFARRQAIRESWGQESNAGNQTVVVRVF
LYLRCRNYSLIDQPDKCAKKPFLLLAIKSLTPHFARRQAIRESWGQESNAGNQTVVVRVF

LLGQTPPEDNHPDLSMLKFESEKHQDILMWNRYRDTFFNLSLKEVLFLRWVSTSCPDTEF
LLGQTPPEDNHPDLSMLKFESEKHQDILMWNRYRDTFFNLSLKEVLFLRWVSTSCPDTEF
LLGQTPPEDNHPDLSMLKFESEKHQDILMWNRYRDTFFNLSLKEVLFLRWVSTSCPDTEF

VFKGDDDVFNTHHILNYLNSLSKTKAKDLFIGDVIHNAGPHRDKKLYYIPEVVYSGLY
VFKGDDDVFNTHHILNYLNSLSKTKAKDLFIGDVIHNAGPHRDKKLYYIPEVVYSGLY
VFKGDDDVFNTHHILNYLNSLSKTKAKDLFIGDVIHNAGPHRDKKLYYIPEVVYSGLY

PPYAGGGGFLYSGHLALRLYHITDQVHLYPIDDVYTMCLQKLGLVPEKHKGFRFTDIEE
PPYAGGGGFLYSGHLALRLYHITDQVHLYPIDDVYTMCLQKLGLVPEKHKGFRFTDIEE
PPYAGGGGFLYSGHLALRLYHITDQVHLYPIDDVYTMCLQKLGLVPEKHKGFRFTDIEE

KNKNNICSYVDLMLVHSRKPQEMIDIWSQLQSAHLKC
KNKNNICSYVDLMLVHSRKPQEMIDIWSQLQSAHLKC
KNKNNICSYVDLMLVHSRKPQEMIDIWSQLQSAHLKC

FIG. 10

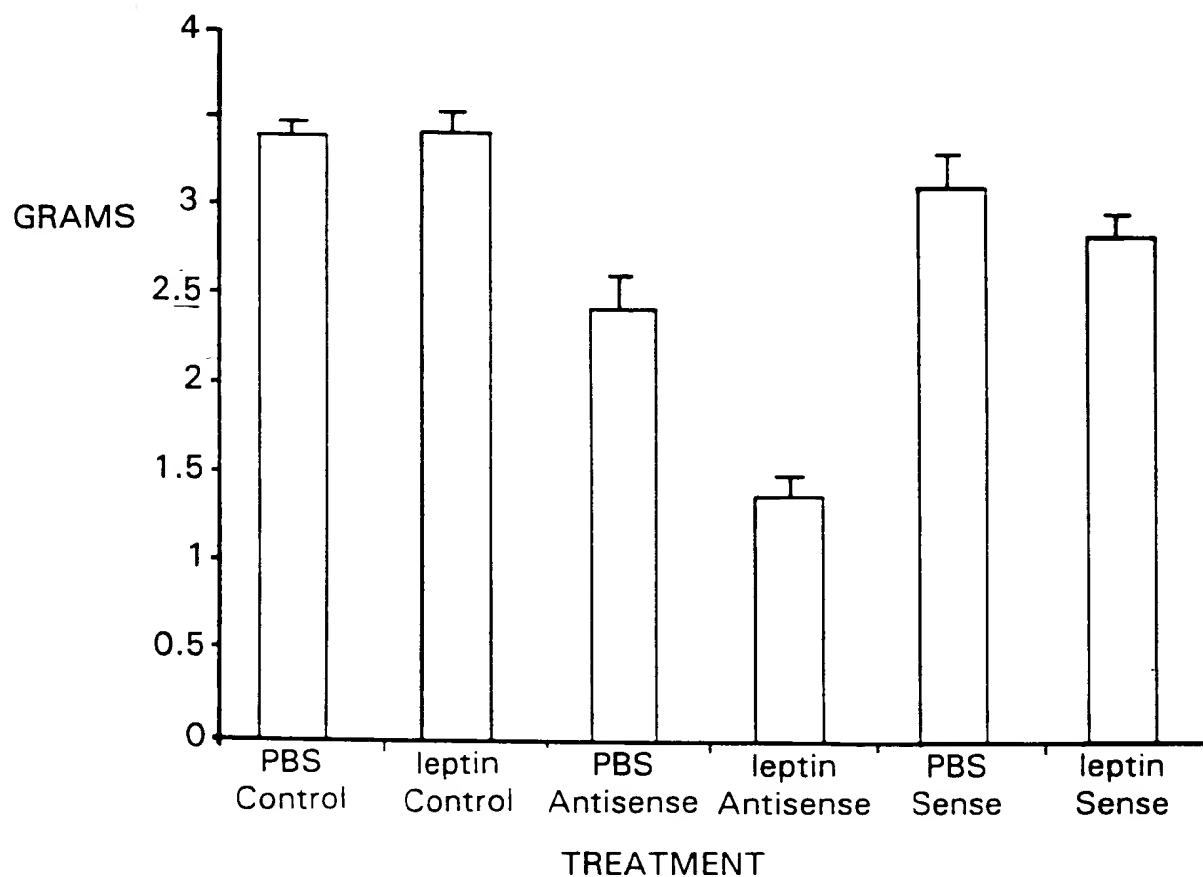
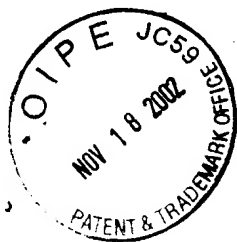


FIG. 11